Supplementary Material

Genome-wide analysis of gene regulatory networks of the FVE-HDA6-FLD complex in Arabidopsis

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Supplememtal Figure 1. HDA6 and FLD physically interacted with FVE.
BiFC assays in tobacco leaves show the interaction between HDA6 and FVE **(A)**, HDA6 and FLD **(B)** or FLD and FVE **(C)** in living cells. HDA6, FVE and FLD were fused with the C terminus (YC) or N terminus (YN) of YFP. Empty vectors (YN and YC) were also co-transfected as the negative control **(D)**.

Supplememtal Figure 2. Heatmap clustering of transposons up-regulated in *hda6-6*, *fve-4* and *fld-6*. Cluster analysis of transposons which were up-regulated in *hda6-6*, *fve-4* and *fld-6*. The transposons represented in at least one of mutants were analyzed. The color bar represents the log2 of the RPKM value.

Supplemental Figure 3. Functional annotation of genes regulated by FVE, FLD, and HDA6. (A-C) Relative number of genes up-regulated in *fve-4*, *fld-6*, and *hda6-6* analyzed by DAVID database. (D-F) Functional classification of genes up-regulated in *fve-4*, *fld-6*, and *hda6-6*.

Supplemental Figure 4. Validation of RNA-sequencing results.
(A-B) Real-time RT-PCR analysis of the expression of ethylene related genes in Col wild type, *hda6-6*, *fld-6* and *fve-4* plants grown under LD conditions for 14 days. (C) Gene involved in transport. (D-H) Genes related to cell wall expansion. The values shown are means ±SD.

Supplemental Figure 5. Scatterplot of Pearson correlation of three RNA-seq replicates for wild-type (Col) and *hda6-6* mutant. The coefficients between replicate 1 and 2, 2 and 3, and 1 and 3 are 0.970057, 0.963591, and 0.96409, respectively, for Col

and 0.972537, 0.96653, 0.96772, respectively, for *hda6-6*.